

-31-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

(ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10

5 (iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
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(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 90067

(v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

20 (A) APPLICATION NUMBER: PCT
(B) FILING DATE: 07-OCT-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

25 (A) NAME: LISA A. HAILE, PH.D.
(B) REGISTRATION NUMBER: P-38,347
(C) REFERENCE/DOCKET NUMBER: FD-3054 PCT

(ix) TELECOMMUNICATION INFORMATION:

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30 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid

-32-

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

5

(B) CLONE: NSC1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

CCGGAATTCA ARGTINGAYTT YGCNGAYATH GGNTGG

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NSC2

20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCT CANGCRCARC TYTCNACNGT CAT

33

25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

-33-

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

(vii) IMMEDIATE SOURCE:

(B) CLONE: NSC3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGAATTCT CANGCRCANG AYTCNACNGT CAT

33

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2322 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

20

(vii) IMMEDIATE SOURCE:

(B) CLONE: Murine GDF-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 126..1553

-34-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	TGGGGTCATC CGGGCTGTCC GAGTCCCACA GGGACAACCTC CAGCCGCGGA CGAGGTGCAC	60
	AGCCAACACT GAGCCCTCCT TGTCTGTTCT CCTGGGCTCA GACCCTTCAC CACCGTTACT	120
5	CAGCC ATG GCT CCA GGT CCT GCT CGG ATC AGC TTG GGG TCC CAG CTG Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu 1 5 10	167
	CTG CCC ATG GTG CCG CTG CTC CTG CTG CTG CGG GGC GCA GGC TGC GGC Leu Pro Met Val Pro Leu Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly 15 20 25 30	215
10	CAC AGG GGC CCC TCA TGG TCC TCA TTG CCC TCG GCA GCT GCC GGT CTG His Arg Gly Pro Ser Trp Ser Ser Leu Pro Ser Ala Ala Ala Gly Leu 35 40 45	263
	CAG GGG GAC AGG GAC TCC CAG CAG TCA CCC GGG GAC GCA GCA GCC GCT Gln Gly Asp Arg Asp Ser Gln Gln Ser Pro Gly Asp Ala Ala Ala Ala 50 55 60	311
15	CTG GGC CCA GGC GCC CAG GAC ATG GTC GCT ATC CAC ATG CTC AGG CTC Leu Gly Pro Gly Ala Gln Asp Met Val Ala Ile His Met Leu Arg Leu 65 70 75	359
	TAT GAG AAG TAC AAC CGA AGA GGT GCT CCA CCG GGA GGA GGC AAC ACC Tyr Glu Lys Tyr Asn Arg Arg Gly Ala Pro Pro Gly Gly Gly Asn Thr 80 85 90	407
20	GTC CGA AGC TTC CGT GCC CGG CTG GAA ATG ATC GAC CAA AAG CCT GTG Val Arg Ser Phe Arg Ala Arg Leu Glu Met Ile Asp Gln Lys Pro Val 95 100 105 110	455
	TAT TTC TTC AAC TTG ACT TCC ATG CAA GAC TCA GAA ATG ATC CTC ACA Tyr Phe Phe Asn Leu Thr Ser Met Gln Asp Ser Glu Met Ile Leu Thr 115 120 125	503
	GCC GCC TTC CAC TTC TAC TCA GAA CCT CCA CGG TGG CCC CGG GCT GGT Ala Ala Phe His Phe Tyr Ser Glu Pro Pro Arg Trp Pro Arg Ala Gly 130 135 140	551
30	GAG GTA TTC TGC AAG CCC CGA GCT AAG AAC GCA TCC TGC CGC CTC CTG Glu Val Phe Cys Lys Pro Arg Ala Lys Asn Ala Ser Cys Arg Leu Leu 145 150 155	599

-35-

	ACC CCA GGG CTG CCT GCA CGC TTG CAC CTA ATC TTC CGC AGT CTT TCC	647
	Thr Pro Gly Leu Pro Ala Arg Leu His Leu Ile Phe Arg Ser Leu Ser	
	160 165 170	
5	CAG AAC ACC GCC ACT CAG GGG CTG CTC CGC GGG GCC ATG GCC CTG ACG	695
	Gln Asn Thr Ala Thr Gln Gly Leu Leu Arg Gly Ala Met Ala Leu Thr	
	175 180 185 190	
	CCT CCA CCA CGT GGC CTG TGG CAG GCC AAG GAC ATC TCC TCA ATC ATC	743
	Pro Pro Pro Arg Gly Leu Trp Gln Ala Lys Asp Ile Ser Ser Ile Ile	
	195 200 205	
10	AAG GCT GCC CGA AGG GAT GGA GAG CTG CTT CTC TCT GCT CAG CTG GAT	791
	Lys Ala Ala Arg Arg Asp Gly Glu Leu Leu Leu Ser Ala Gln Leu Asp	
	215 220	
	ACT GAG AAG GAC CCC GGA GTG CCA CGG CCC AGT TCC CAC ATG CCC	839
	Thr Glu Lys Asp Pro Gly Val Pro Arg Pro Ser Ser His Met Pro	
15	225 230 235	
	TAT ATC CTT GTC TAC GCC AAT GAC CTG GCC ATC TCC GAA CCC AAC AGT	887
	Tyr Ile Leu Val Tyr Ala Asn Asp Leu Ala Ile Ser Glu Pro Asn Ser	
	240 245 250	
20	GTA GCA GTG TCG CTA CAG AGA TAC GAC CCA TTT CCA GCT GGA GAC TTT	935
	Val Ala Val Ser Leu Gln Arg Tyr Asp Pro Phe Pro Ala Gly Asp Phe	
	255 260 265 270	
	GAG CCT GGA GCA GCC CCC AAC AGC TCA GCT GAT CCC CGC GTG CGC AGG	983
	Glu Pro Gly Ala Ala Pro Asn Ser Ser Ala Asp Pro Arg Val Arg Arg	
	275 280 285	
25	GCG GCT CAG GTG TCA AAA CCC CTG CAA GAC AAT GAA CTG CCG GGG CTG	1031
	Ala Ala Gln Val Ser Lys Pro Leu Gln Asp Asn Glu Leu Pro Gly Leu	
	290 295 300	
	GAT GAA AGA CCA GCG CCT GCC CTG CAT GCC CAG AAT TTC CAC AAG CAC	1079
	Asp Glu Arg Pro Ala Pro Ala Leu His Ala Gln Asn Phe His Lys His	
30	305 310 315	
	GAG TTC TGG TCC AGT CCT TTC CGG GCA CTG AAA CCC CGC ACG GCG CGC	1127
	Glu Phe Trp Ser Ser Pro Phe Arg Ala Leu Lys Pro Arg Thr Ala Arg	
	320 325 330	

-36-

AAA GAC CGC AAG AAG AAG GAC CAG GAC ACA TTC ACC GCC GCC TCC TCT 1175
 Lys Asp Arg Lys Lys Lys Asp Gln Asp Thr Phe Thr Ala Ala Ser Ser
 335 340 345 350

5 CAG GTG CTG GAC TTT GAC GAG AAG ACG ATG CAG AAA GCC AGG AGG CGG 1223
 Gln Val Leu Asp Phe Asp Glu Lys Thr Met Gln Lys Ala Arg Arg Arg
 355 360 365

CAG TGG GAT GAG CCC CGG GTC TGC TCC AGG AGG TAC CTG AAG GTG GAT 1271
 Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg Tyr Leu Lys Val Asp
 370 375 380

10 TTT GCA GAC ATC GGG TGG AAT GAA TGG ATC ATC TCT CCC AAA TCC TTT 1319
 Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile Ser Pro Lys Ser Phe
 385 390 395

15 GAC GCC TAC TAC TGT GCT GGG GCC TGC GAG TTC CCC ATG CCC AAG ATT 1367
 Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe Pro Met Pro Lys Ile
 400 405 410

GTC CGC CCA TCC AAC CAT GCC ACC ATC CAG AGC ATC GTC AGA GCT GTG 1415
 Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val
 415 420 425 430

20 GGC ATT GTC CCT GGC ATC CCA GAG CCA TGC TGT GTT CCA GAC AAG ATG 1463
 Gly Ile Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Asp Lys Met
 435 440 445

AAC TCC CTT GGA GTC CTT TTC CTG GAT GAA AAT CGG AAT GCG GTT CTG 1511
 Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn Arg Asn Ala Val Leu
 450 455 460

25 AAG GTG TAC CCC AAT ATG TCC GTA GAG ACC TGT GCC TGT CGG 1553
 Lys Val Tyr Pro Asn Met Ser Val Glu Thr Cys Ala Cys Arg
 465 470 475

TAAGATGGCT TCAAGATAGA AGACAGACCT GCTTCATCCC TGCCCTGCAG AGTGGCAATC 1613
 TTGGAGCCAG GGAAGTGGCT CGGGGAGGTT CCAGGTGCTA GACAGAGCTT ACAGGCAGCC 1673

30 CTGCTGGGAC CAAGAAAGAT CTGCCCACCA CATCGCAATT CTTCAATTCT TCCGTGCTGG 1733
 TGGTAGCTCT GTAAAGACGT GTTGAGTTCC TGGAAGAAAT CTGGAATTAA CTGTGGTCTG 1793
 CAATTTGCCC ATCATCCCTG CCCACACTTT TCAAGGCCTA GAAATAACGT GTGTCCTCAA 1853

-37-

ATGTCAACTC CAGGCATTTG TCCTCTCAAA ACCTAGAAAAG ACTATGCAAA TCTTGGGGTA 1913
 CTCACCCCCC CCATGGCAGT TTAAATGCTG TTTTAAAACC CTCAGGCTGC ATTCTAGAAA 1973
 CAGGGCCTAA CCCATGGCAC GAGTGAGTAT TTTCTCTTAC GTTTCACCTAC ACGTGCTTTT 2033
 ATACATGCAG TATGCACATG TAATCACGGT TGATTTCTTC TTTTAATATA TGTATTTCTA 2093
 5 TTTCAAAGCA AAACGGAGAG AGTCGATCCC ATCCCCTGCA GAGGTAATAA TGCAAGTTAG 2153
 GTGTGGGTTG TCTAAGCATG TGTATGGAAA TAATACATAC AGTAATATGC TGAATACTA 2213
 AAAAAGTAAC CAAGATTTTA TATTTTGTGTA AATTATACTT TGTATACTGT AGATTGTGAG 2273
 TGTCTGTGT TTTTATGGAA AGCTAATAAA TTAAAGGTGC GGAGGTATC 2322

(2) INFORMATION FOR SEQ ID NO:5:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu Leu Pro
 1 5 10 15

Met Val Pro Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly His Arg
 20 25 30

20

Gly Pro Ser Trp Ser Ser Leu Pro Ser Ala Ala Ala Gly Leu Gln Gly
 35 40 45

Asp Arg Asp Ser Gln Gln Ser Pro Gly Asp Ala Ala Ala Leu Gly
 50 55 60

25

Pro Gly Ala Gln Asp Met Val Ala Ile His Met Leu Arg Leu Tyr Glu
 65 70 75 80

Lys Tyr Asn Arg Arg Gly Ala Pro Pro Gly Gly Gly Asn Thr Val Arg
 85 90 95

-38-

Ser Phe Arg Ala Arg Leu Glu Met Ile Asp Gln Lys Pro Val Tyr Phe
 100 105 110

Phe Asn Leu Thr Ser Met Gln Asp Ser Glu Met Ile Leu Thr Ala Ala
 115 120 125

5 Phe His Phe Tyr Ser Glu Pro Pro Arg Trp Pro Arg Ala Gly Glu Val
 130 135 140

Phe Cys Lys Pro Arg Ala Lys Asn Ala Ser Cys Arg Leu Leu Thr Pro
 145 150 155 160

10 Gly Leu Pro Ala Arg Leu His Leu Ile Phe Arg Ser Leu Ser Gln Asn
 165 170 175

Thr Ala Thr Gln Gly Leu Leu Arg Gly Ala Met Ala Leu Thr Pro Pro
 180 185 190

Pro Arg Gly Leu Trp Gln Ala Lys Asp Ile Ser Ser Ile Ile Lys Ala
 195 200 205

15 Ala Arg Arg Asp Gly Glu Leu Leu Leu Ser Ala Gln Leu Asp Thr Gly
 210 215 220

Glu Lys Asp Pro Gly Val Pro Arg Pro Ser Ser His Met Pro Tyr Ile
 225 230 235 240

20 Leu Val Tyr Ala Asn Asp Leu Ala Ile Ser Glu Pro Asn Ser Val Ala
 245 250 255

Val Ser Leu Gln Arg Tyr Asp Pro Phe Pro Ala Gly Asp Phe Glu Pro
 260 265 270

Gly Ala Ala Pro Asn Ser Ser Ala Asp Pro Arg Val Arg Arg Ala Ala
 275 280 285

25 Gln Val Ser Lys Pro Leu Gln Asp Asn Glu Leu Pro Gly Leu Asp Glu
 290 295 300

Arg Pro Ala Pro Ala Leu His Ala Gln Asn Phe His Lys His Glu Phe
 305 310 315 320

30 Trp Ser Ser Pro Phe Arg Ala Leu Lys Pro Arg Thr Ala Arg Lys Asp
 325 330 335

-39-

Arg Lys Lys Lys Asp Gln Asp Thr Phe Thr Ala Ala Ser Ser Gln Val
 340 345 350

Leu Asp Phe Asp Glu Lys Thr Met Gln Lys Ala Arg Arg Arg Gln Trp
 355 360 365

5 Asp Glu Pro Arg Val Cys Ser Arg Arg Tyr Leu Lys Val Asp Phe Ala
 370 375 380

Asp Ile Gly Trp Asn Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala
 385 390 395 400

10 Tyr Tyr Cys Ala Gly Ala Cys Glu Phe Pro Met Pro Lys Ile Val Arg
 405 410 415

Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Ile
 420 425 430

Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Asp Lys Met Asn Ser
 435 440 445

15 Leu Gly Val Leu Phe Leu Asp Glu Asn Arg Asn Ala Val Leu Lys Val
 450 455 460

Tyr Pro Asn Met Ser Val Glu Thr Cys Ala Cys Arg
 465 470 475

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-10

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..120

30

-40-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Lys Ser Met Gln Lys Ala Arg Arg Arg Gln Trp Asp Glu Pro Arg
 1 5 10 15
 Val Cys Ser Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
 5 20 25 30
 Asn Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ala
 35 40 45
 Gly Ala Cys Glu Phe Pro Met Pro Lys Ile Val Arg Pro Ser Asn His
 50 55 60
 Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Ile Val Pro Gly Ile
 10 65 70 75 80
 Pro Glu Pro Cys Cys Val Pro Asp Lys Met Asn Ser Leu Gly Val Leu
 85 90 95
 Phe Leu Asp Glu Asn Arg Asn Ala Val Leu Lys Val Tyr Pro Asn Met
 15 100 105 110
 Ser Val Glu Thr Cys Ala Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:7:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-1

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..123

-41-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly
 1 5 10 15
 Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp
 5 20 25 30
 His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln
 35 40 45
 Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro
 50 55 60
 Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro
 10 65 70 75 80
 Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile
 85 90 95
 Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr
 15 100 105 110
 Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:8:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-3

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..118

-42-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Lys Arg Arg Ala Ala Ile Ser Val Pro Lys Gly Phe Cys Arg Asn
 1 5 10 15
 Phe Cys His Arg His Gln Leu Phe Ile Asn Phe Gln Asp Leu Gly Trp
 5 20 25 30
 His Lys Trp Val Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His
 35 40 45
 Gly Glu Cys Pro Phe Ser Met Thr Thr Tyr Leu Asn Ser Ser Asn Tyr
 50 55 60
 Ala Phe Met Gln Ala Leu Met His Met Ala Asp Pro Lys Val Pro Lys
 10 65 70 75 80
 Ala Val Cys Val Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln
 85 90 95
 Asp Ser Asp Lys Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val
 15 100 105 110
 Asp Glu Cys Gly Cys Gly
 115

(2) INFORMATION FOR SEQ ID NO:9:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-9

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

-43-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Phe Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn
 1 5 10 15
 Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp
 5 20 25 30
 Asp Asn Trp Ile Val Ala Pro His Arg Tyr Asn Pro Arg Tyr Cys Lys
 35 40 45
 Gly Asp Cys Pro Arg Ala Val Arg His Arg Tyr Gly Ser Pro Val His
 50 55 60
 Thr Met Val Gln Asn Ile Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro
 10 65 70 75 80
 Arg Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr
 85 90 95
 Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile
 15 100 105 110
 Ala Thr Arg Cys Thr Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:10:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: BMP-2

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..118

-44-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
 1 5 10 15
 Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
 5 20 25 30
 Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
 35 40 45
 Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
 50 55 60
 Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
 10 65 70 75 80
 Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
 85 90 95
 Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
 15 100 105 110
 Glu Gly Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: BMP-4

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..118

-45-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
1 5 10 15

Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
20 25 30

Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
35 40 45

Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
50 55 60

10 Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
65 70 75 80

Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
85 90 95

15 Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
100 105 110

Glu Gly Cys Gly Cys Arg
115

(2) INFORMATION FOR SEQ ID NO:12:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
(B) CLONE: Vgr-1

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..119

-46-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Arg Gly Ser Gly Ser Ser Asp Tyr Asn Gly Ser Glu Leu Lys Thr
 1 5 10 15
 Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
 5 20 25 30
 Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp
 35 40 45
 Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 50 55 60
 Ala Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro
 10 65 70 75 80
 Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
 85 90 95
 Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
 15 100 105 110
 Val Arg Ala Cys Gly Cys His
 115

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: OP-1

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

-47-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
 1 5 10 15
 Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
 5 20 25 30
 Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu
 35 40 45
 Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His
 50 55 60
 Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro
 10 65 70 75 80
 Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr
 85 90 95
 Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
 15 100 105 110
 Val Arg Ala Cys Gly Cys His
 115

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: BMP-5

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

-48-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln
 1 5 10 15
 Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
 5 20 25 30
 Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp
 35 40 45
 Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 50 55 60
 Ala Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro
 10 65 70 75 80
 Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
 85 90 95
 Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
 15 100 105 110
 Val Arg Ser Cys Gly Cys His
 115

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: OP-2

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

-49-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln
 1 5 10 15
 Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
 5 20 25 30
 Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu
 35 40 45
 Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His
 50 55 60
 Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro
 10 65 70 75 80
 Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr
 85 90 95
 Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg Asn Met Val
 15 100 105 110
 Val Lys Ala Cys Gly Cys His
 115

(2) INFORMATION FOR SEQ ID NO:16:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: BMP-3

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..120

-50-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
 1 5 10 15
 Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
 5 20 25 30
 Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
 35 40 45
 Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
 50 55 60
 Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
 10 65 70 75 80
 Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
 85 90 95
 Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
 15 100 105 110
 Thr Val Glu Ser Cys Ala Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:17:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: MIS

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..116

-51-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
 1 5 10 15
 Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
 5 20 25 30
 Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
 35 40 45
 Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
 50 55 60
 10 Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
 65 70 75 80
 Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
 85 90 95
 15 Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
 100 105 110
 Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:18:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: Inhibin-alpha

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..122

-52-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala
 1 5 10 15

Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp
 5 20 25 30

Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His
 35 40 45

Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro
 50 55 60

Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala
 10 65 70 75 80

Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val
 85 90 95

Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro
 15 100 105 110

Asn Leu Leu Thr Gln His Cys Ala Cys Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: Inhibin-beta-A

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..121

-53-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile Cys
 1 5 10 15
 Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp
 20 25 30
 Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu
 35 40 45
 Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His
 50 55 60
 Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala
 65 70 75 80
 Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met
 85 90 95
 Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln Asn
 100 105 110
 Met Ile Val Glu Glu Cys Gly Cys Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Inhibin-beta-B

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..120

-54-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys
 1 5 10 15
 Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp
 5 20 25 30
 Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser
 35 40 45
 Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His
 50 55 60
 Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr
 10 65 70 75 80
 Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu
 85 90 95
 Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met
 15 100 105 110
 Ile Val Glu Glu Cys Gly Cys Ala
 115 120

(2) INFORMATION FOR SEQ ID NO:21:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: Nodal

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..118

-55-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Trp Gly Arg Arg Gln Arg Arg His His Leu Pro Asp Arg Ser Gln
 1 5 10 15
 Leu Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp
 5 20 25 30
 Gly Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu
 35 40 45
 Gly Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His
 50 55 60
 Ala Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro
 10 65 70 75 80
 Ser Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr
 85 90 95
 Val Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val
 15 100 105 110
 Glu Glu Cys Gly Cys Leu
 115

(2) INFORMATION FOR SEQ ID NO:22:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: TGF-beta-1

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..114

-56-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn
 1 5 10 15
 Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp
 5 20 25 30
 Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly
 35 40 45
 Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu
 50 55 60
 Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys
 10 65 70 75 80
 Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg
 85 90 95
 Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys
 15 100 105 110
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:23:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: TGF-beta-2

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..114

-57-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn
 1 5 10 15
 Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp
 5 20 25 30
 Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly
 35 40 45
 Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
 50 55 60
 Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 10 65 70 75 80
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
 85 90 95
 Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
 15 100 105 110
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:24:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: TGF-beta-3

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..114

-58-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

[illegible]

(2) INFORMATION FOR SEQ ID NO:25:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
(B) CLONE: Human GDF-10

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(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..115
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-59-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Ala Arg Arg Lys Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg
 1 5 10 15
 Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile
 5 20 25 30
 Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe
 35 40 45
 Pro Met Pro Lys Ile Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser
 50 55 60
 10 Ile Val Arg Ala Val Gly Ile Ile Pro Gly Ile Pro Glu Pro Cys Cys
 65 70 75 80
 Val Pro Asp Lys Met Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn
 85 90 95
 15 Arg Asn Val Val Leu Lys Val Tyr Pro Asn Met Ser Val Asp Thr Cys
 100 105 110
 Ala Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:26:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:
 (B) CLONE: Murine GDF-10

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..115

-60-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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Lys Ala Arg Arg Lys Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg
1             5             10             15

Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile
5           20           25           30

Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe
          35           40           45

Pro Met Pro Lys Ile Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser
      50           55           60

Ile Val Arg Ala Val Gly Ile Val Pro Gly Ile Pro Glu Pro Cys Cys
10    65           70           75           80

Val Pro Asp Lys Met Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn
          85           90           95

Arg Asn Ala Val Leu Lys Val Tyr Pro Asn Met Ser Val Glu Thr Cys
15    100          105          110

Ala Cys Arg
      115

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